

FIGURE 1

TAAACAGCTACAATATTCCAGGGCCAGTCACTTGCCATTTCTCATAACAGCGTCAGAGAGAAAGAACTGACTGA
AACGTTTGAGATGAAGAAAAGTTCTCCTCCTGATCACAGCCATCTTGGCAGTGGCTGTTGGTTTTCCAGTCTCTCA
AGACCAGGAACGAGAAAAAAGAAGTATCAGTGACAGCGATGAATTAGCTTCAGGGTTTTTTGTGTTCCCTTACCC
ATATCCATTTGCCCCACTTCCACCAATTCCATTTCCAAGATTTCCATGGTTTAGACGTAATTTTCCTATTCCAAT
ACCTGAATCTGCCCCTACAACCTCCCCTTCCTAGCGAAAAGTAAACAAGAAGGATAAGTCACGATAAACCTGGTCA
CCTGAAATTGAAATTGAGCCACTTCCTTGAAGAATCAAAATTCCTGTTAATAAAAGAAAAACAAATGTAATTGAA
ATAGCACACAGCATTCTCTAGTCAATATCTTTAGTGATCTTCTTAATAAACATGAAAGCAAAGATTTTGGTTTC
TTAATTTCCACA

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FIGURE 2

GGAGAGAGGCGCGCGGGTGAAAGGCGCATTGATGCAGCCTGCGGCGGCCTCGGAGCGCGCGGAGCCAGACGCTG
ACCACGTTCTCTCCTCGGTCTCCTCCGCCTCCAGCTCCGCGCTGCCCGGCAGCCGGGAGCC**ATG**CGACCCAGG
GCCCCGCCGCTCCCCGCAGCGGCTCCGCGGCCTCCTGCTGCTCCTGCTGCTGCAGCTGCCCGCGCCGTCGAGCG
CCTCTGAGATCCCCAAGGGGAAGCAAAGGCGCAGCTCCGGCAGAGGGAGGTGGTGGACCTGTATAATGGAATGT
GCTTACAAGGGCCAGCAGGAGTGCCTGGTCGAGACGGGAGCCCTGGGGCCAATGTTATTCCGGGTACACCTGGGA
TCCCAGGTCCGGATGGATTCAAAGGAGAAAAGGGGAATGTCTGAGGGAAAGCTTTGAGGAGTCTGGACACCCA
ACTACAAGCAGTGTTCATGGAGTTCATTGAATTATGGCATAGATCTTGGGAAAATTGCGGAGTGTACATTTACAA
AGATGCGTTCAAATAGTGCTCTAAGAGTTTTGTTCAGTGGCTCACTTCGGCTAAAATGCAGAAATGCATGCTGTC
AGCGTTGGTATTTACATTCAATGGAGCTGAATGTTTCAGGACCTCTTCCCATTTGAAGCTATAATTTATTTGGACC
AAGGAAGCCCTGAAATGAATTCAACAATTAATATTCATCGCACTTCTTCTGTGGAAGGACTTTGTGAAGGAATTG
GTGCTGGATTAGTGGATGTTGCTATCTGGGTTGGCACTTGTTCAGATTACCCAAAAGGAGATGCTTCTACTGGAT
GGAATTCAGTTTCTCGCATCATTATTGAAGAACTACCAAAA**TAA**ATGCTTTAATTTTCATTTGCTACCTCTTTTT
TTATTATGCCTTGGAATGGTTCACTTAAATGACATTTTAAATAAGTTTATGTATACATCTGAATGAAAAGCAAAG
CTAAATATGTTTACAGACCAAAGTGTGATTTACACTGTTTTTAAATCTAGCATTATTCATTTTGCTTCAATCAA
AAGTGGTTTCAATATTTTTTTTTTAGTTGGTTAGAATACTTCTTCATAGTCACATTCTCTCAACCTATAATTTGGA
ATATTGTTGTGGTCTTTTGTTTTTTCTCTTAGTATAGCATTTTTAAAAAAATATAAAAGCTACCAATCTTTGTAC
AATTTGTAAATGTTAAGAATTTTTTTTTATATCTGTAAATAAAAATTATTTCCAACA

FIGURE 3

GCCAGGGGAAGAGGGTGATCCGACCCGGGGAAGGTCGCTGGGCAGGGCGAGTTGGGAAAGCGGCAGCCCCGCCG
 CCCCCGAGCCCCCTTCTCCTCCTTTCTCCACGTCCTATCTGCCTCTCGCTGGAGGCCAGGCCGTGCAGCATCGA
 AGACAGGAGGAACTGGAGCCTCATTGGCCGGCCCGGGGCGCCGGCCTCGGGCTTAAATAGGAGCTCCGGGCTCTG
 GCTGGGACCCGACCGCTGCCGGCCGCGCTCCCGCTGCTCCTGCCGGGTGATGGAAAAACCCAGCCCGGCCGCCG
 CCTGGGCAAGGCCCTCTGCGCTCTCCTCCTGGCCACTCTCGGCGCCGCCAGCCTCTTGGGGGAGAGTCCAT
 CTGTTCCGCCAGAGCCCCGGCCAAATACAGCATCACCTTCACGGGCAAGTGGAGCCAGACGGCCTTCCCCAAGCA
 GTACCCCTGTTCGCCCCCTGCGCAGTGGTCTTCGCTGCTGGGGGCCGCGCATAGCTCCGACTACAGCATGTG
 GAGGAAGAACCAGTACGTAGTAACGGGCTGCGCGACTTTGCGGAGCGCGCGAGGCCTGGGCGCTGATGAAGGA
 GATCGAGGCGGCGGGGAGGCGCTGCAGAGCGTGCACGAGGTGTTTTCGGCGCCCGCCGTCCCCAGCGGCACCGG
 GCAGACGTTCGGCGGAGCTGGAGGTGCAGCGCAGGCACTCGCTGGTCTCGTTTGTGGTGCGCATCGTGCCAGCCC
 CGACTGGTTCGTGGGCGTGGACAGCCTGGACCTGTGCGACGGGGACCGTTGGCGGGAACAGGCGGCGCTGGACCT
 GTACCCCTACGACGCCGGGACGGACAGCGGCTTACCTTCTCCTCCCCAACTTCGCCACCATCCCGCAGGACAC
 GGTGACCGAGATAACGTCTCCTCTCCCAGCCACCCGGCCAACTCCTTCTACTACCGCGGGCTGAAGGCCCTGCC
 TCCCATCGCCAGGGTGACACTGCTGCGGCTGCGACAGAGCCCCAGGGCCTTCATCCCTCCCGCCCCAGTCTGCC
 CAGCAGGGACAATGAGATTGTAGACAGCGCCTCAGTTCCAGAAACGCCGCTGGACTGCGAGGTCTCCCTGTGGTC
 GTCCTGGGGACTGTGCGGAGGCCACTGTGGGAGGCTCGGGACCAAGAGCAGGACTCGCTACGTCCGGGTCCAGCC
 CGCCAACAACGGGAGCCCCCTGCCCGAGCTCGAAGAAGAGGCTGAGTGCGTCCCTGATAACTGCGTCTTAAGACCA
 GAGCCCCGAGCCCCCTGGGGCCCCCGGAGCCATGGGGTGTGCGGGGCTCCTGTGCAGGCTCATGCTGCAGGCGG
 CCGAGGGCACAGGGGGTTTTGCGGCTGCTCCTGACCGCGGTGAGGCCGCGCCGACCATCTCTGCACTGAAGGGCCC
 TCTGGTGGCCGGCACGGGCATTGGGAAACAGCCTCCTCCTTTCCCAACCTTGCTTCTTAGGGGCCCCCGTGTCCC
 GTCTGCTCTCAGCCTCCTCCTCCTGCAGGATAAAGTCATCCCCAAGGCTCCAGCTACTCTAAATTATGTCTCCTT
 ATAAGTTATTGCTGCTCCAGGAGATTGTCCTTCATCGTCCAGGGGCTGGCTCCACGTGGTTGCAGATACCTCA
 GACCTGGTGCTCTAGGCTGTGCTGAGCCCACTCTCCCGAGGGCGCATCCAAGCGGGGGCCACTTGAGAAGTGAAT
 AAATGGGGCGGTTTTCGGAAGCGTCAGTGTTTCCATGTTATGGATCTCTCTGCGTTTGAATAAAGACTATCTCTGT
 TGCTCACAAA

FIGURE 4

GAGGAACCTACCGGTACCGGCCGCGCGCTGGTAGTCGCCGGTGTGGCTGCACCTACCAATCCCGTGCGCCGCGG
 CTGGGCCGTCGGAGAGTGCCTGTGCTTCTCTCCTGCACGCGGTGCTTGGGCTCGGCCAGGCGGGGTCCGCCGCCA
 GGGTTTGAGGATGGGGGAGTAGCTACAGGAAGCGACCCCGCATGGCAAGGTATATTTTTGTGGAATGAAAAGGA
 AGTATTAGAAATGAGCTGAAGACCATTACAGATTAATATTTTTGGGGACAGATTGTGATGCTTGATTACCCCT
 TGAAGTAATGTAGACAGAAGTTCTCAAATTTGCATATTACATCAACTGGAACCAGCAGTGAATCTTAATGTTTAC
 TTAAATCAGAACTTGCATAAGAAAGAGAATGGGAGTCTGGTTAAATAAAGATGACTATATCAGAGACTTGAAAAG
 GATCATTCTCTGTTTTCTGATAGTGTATATGGCCATTTTAGTGGGCACAGATCAGGATTTTTACAGTTTACTTGG
 AGTGTCCAAAACCTGCAAGCAGTAGAGAAAATAAGACAAGCTTTCAAGAAATTGGCATTGAAGTTACATCCTGATAA
 AAACCCGAATAACCCAAATGCACATGGCGATTTTTTAAAAATAAATAGAGCATATGAAGTACTCAAAGATGAAGA
 TCTACGGAAAAAGTATGACAAATATGGAGAAAAGGGACTTGAGGATAATCAAGGTGGCCAGTATGAAAGCTGGAA
 CTATTATCGTTATGATTTTTGGTATTTATGATGATGATCCTGAAATCATAACATGGAAAGAAGAGAATTTGATGC
 TGCTGTTAATTTCTGGAGAAGTGTGGTTTGTAAATTTTTACTCCCCAGGCTGTTCACTGCCATGATTTAGCTCC
 CACATGGAGAGACTTTGCTAAAGAAGTGGATGGGTACTTCAATGGAGCTGTTAACTGTGATGATAGAAT
 GCTTTGCCGAATGAAAGGAGTCAACAGCTATCCAGTCTCTTCAATTTTTCGGTCTGGAATGGCCCCAGTGAAATA
 TCATGGAGACAGATCAAAGGAGAGTTTAGTGAGTTTTGCAATGCAGCATGTTAGAAGTACAGTGACAGAAGTTTG
 GACAGGAAATTTGTCAACTCCATACAACTGCTTTTGCTGCTGGTATTTGGCTGGCTGATCACTTTTTGTTCAAAA
 AGGAGGAGATTGTTTGACTTCACAGACACGACTCAGGCTTAGTGGCATGTTGTTTCTCAACTCATTGGATGCTAA
 AGAAATATATTTGGAAGTAATACATAATCTTCCAGATTTTGAAGTACTTTCCGCAACACACTAGAGGATCGTTT
 GGCTCATCATCGGTGGCTGTTATTTTTTTCATTTTGGAAAAAATGAAAATTCAAATGATCCTGAGCTGAAAAACT
 AAAAAGTCTACTTAAAAATGATCATATTCAAGTTGGCAGGTTTACTGTTCTCTGCACCAGACATCTGTAGTAA
 TCTGTATGTTTTTCAAGCTCTCTAGCAGTATTTAAAGGACAAGGAACCAAGAAATATGAAATTCATCATGGAAA
 GAAGATTCTATATGATATACTTGCCTTTGCCAAAGAAAGTGTGAATTTCTCATGTTACCACGCTTGGACCTCAAAA
 TTTTCTGCCAATGACAAAGAACCATGGCTTGTGATTTCTTTGCCCCCTGGTGTCCACCATGTGAGCTTTACT
 ACCAGATTACGAAGAGCATCAAATCTTCTTTATGGTCAGCTTAAGTTTGGTACACTAGATTGTACAGTTTCATGA
 GGGACTCTGTAACATGTATAACATTCAAGGCTTATCCAACAACAGTGGTATTCAACCAGTCCAACATTCATGAGTA
 TGAAGGACATCACTCTGCTGAACAAATCTTGGAGTTCATAGAGGATCTTATGAATCCTTCAGTGGTCTCCCTTAC
 ACCCACCACCTTCAACGAAGTATGTTACACAAAGAAAACACAACGAAGTCTGGATGGTTGATTTCTATTCTCCGTG
 GTGTCTATCCTTGCCAAGTCTTAATGCCAGAATGGAAAAGAAATGGCCCCGACATTAAGTGGACTGATCAACGTGGG
 CAGTATAGATTGCCAACAGTATCATTCTTTTTGTGCCCAGGAAAACGTTCAAAGATACCCCTGAGATAAGATTTTT
 TCCCCCAAAATCAAATAAAGCTTATCAGTATCAGATTACAATGGTTGGAATAGGGATGCTTATTCCTGAGAAT
 CTGGGGTCTAGGATTTTTTACCTCAAGTATCCACAGATCTAACACCTCAGACTTTTCACTGAAAAAGTTCTACAAGG
 GAAAAATCATTGGGTGATTGATTTCTATGCTCCTTGGTGTGGACCTTGCCAGAATTTTGCTCCAGAATTTGAGCT
 CTTGGCTAGGATGATTAAAGGAAAAGTGAAGCTGGAAAAGTAGACTGTCAGGCTTATGCTCAGACATGCCAGAA
 AGCTGGGATCAGGGCCTATCCAAGTGTAAAGTTTATTTCTACGAAAGAGCAAAGAGAAATTTTCAAGAAGAGCA
 GATAAATACCAGAGATGCAAAAGCAATCGCTGCCTTAATAAGTGAAAATTTGAAAACCTCCGAAATCAAGGCAA
 GAGGAATAAGGATGAAGTTTGAATAATGTTGAAGATGAAGAAAAAGTTTAAAAGAAATTTCTGACAGATGACATCAG
 AAGACACCTATTTAGAATGTTACATTTATGATGGGAATGAATGAACATTATCTTAGACTTGCAGTTGTACTGCCA
 GAATTATCTACAGCACTGGTGTAAAAGAAGGGTCTGCAAACTTTTTCTGTAAAGGGCCGGTTTATAAATATTTTA
 GACTTTGCAAGGCTATAATATATGGTTTACACATGAGAACAAGAATAGAGTCATCATGATTTCTTTGTTATTTGCT
 TTTAACACCTTTAAAAAATATTTAAACGATTTCTAGCTCAGAGCCATACAAAAGTAGGCTGGATTCAAGTCCATG
 GACCATAGATTGCTGTCCCCCTCGACGGACTTATAATGTTTCAAGTGGCTGGCTTGAACATGAGTCTGCTGTGCT
 ATCTACATAAATGTCTAAGTTGTATAAAGTCCACTTTCCCTTCACGTTTTTTGGCTGACCTGAAAAGAGGTAAGT
 TAGTTTTTGGTCACTTGTCTCCTAAAAATGCTATCCCTAACCATATATTTATATTTTCGTTTTTAAAAACACCCAT
 GATGTGGCACAGTAACAAACCCCTGTTATGCTGTATTATTATGAGGAGATTTCTCATTTGTTTTCTTTCTCTCA
 AAGTTGAAAAAATGCTTTTAAATTTTACAGCCGAGAAACAGTGCAGCAGTATATGTGCACACAGTAAGTACAC
 AAATTTGAGCAACAGTAAGTGCACAAATTTCTGTAGTTTGTGTATCATCCAGGAAAACCTGAGGGAAAAAATTA
 TAGCAATTAAGTGGCATTGTAGAGTATCCTAAATATGTTATCAAGTATTTAGAGTTCTATATTTTAAAGATATA
 TGTGTTTATGATTTTCTGAAATTTGCTTTTATAGAAATTTTCCACTGATAGTTGATTTTTTGGGCATCTAATAT
 TTACATATTTGCTTCTGAAGTTTGTGTTTACCTGTATCCTTTATTTACATTTGGGTTTTTCTTTTATAGTTTGG
 TTTTTCACCTCTGTCCAGTCTATTTATTTTCAAATAGGAAAAATTTTACAGGTTGTTTTACTGTAGCTTAT
 AATGATACGTGAGTTATTTCCAGTTTACTAGTTTACTGTAGAGGGCTGCCTTTTTCAGATAAATATTGACATAATA
 ACTGAAGTTATTTTTATAAGAAAATCAAGTATATAAATCTAGGAAAGGGATCTTCTAGTTTCTGTGTTGTTTGA
 CTCAAAGAAATCACAATTTTGTGAGTAACATGATGTTTGTAGTTATAATTCAGAGTGTACAGAATGGTAAAAAT
 CCAATCAGTCAAAGAGGTCAATGAATTTAAAGGCTTGCAACTTTTTCAAAAAAAAAAAAAAAAAA

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FIGURE 5

GGCAACATGGCTCAGCAGGCTTGCCCCAGAGCCATGGCAAAGAATGGACTTGTAATTTGCATCCTGGTGATCACC
 TTACTCCTGGACCAGACCACCAGCCACACATCCAGATTAAAAGCCAGGAAGCACAGCAAACGTCGAGTGAGAGAC
 AAGGATGGAGATCTGAAGACTCAAATTGAAAAGCTCTGGACAGAAGTCAATGCCTTGAAGGAAATTCAAGCCCTG
 CAGACAGTCTGTCTCCGAGGCACTAAAGTTCACAAGAAATGCTACCTTGCTTCAGAAGGTTTGAAGCATTTCAT
 GAGGCCAATGAAGACTGCATTTCCAAAGGAGGAATCCTGGTTATCCCCAGGAACCTCGACGAAATCAACGCCCTC
 CAAGACTATGGTAAAAGGAGCCTGCCAGGTGTCAATGACTTTTGGCTGGGCATCAATGACATGGTCACGGAAGGC
 AAGTTTGTGACGTCAACGGAATCGCTATCTCCTTCCTCAACTGGGACCGTGCACAGCCTAACGGTGGCAAGCGA
 GAAACTGTGTCTGTCTCCCAATCAGCTCAGGGCAAGTGGAGTGATGAGGCCCTGTGCGCAGCAGCAAGAGATAC
 ATATGCGAGTTCAACATCCCTAAATTAGGCTTTTCTCCAATGTGTCTCCTCAAGCAAGATTATCATAACTTATAGG
 TTCATGATCTCTAAGATCAAGTAAAAATCATAATTTTTACTTATTAAAAAATTGCAACACAAGATCAATGTCCAT
 AGCAATATGATAGCATCAGCCAATTTTGCTAACACATTTCTTTGGGATTTTGCCCTTCCTGGGGTATAGGGGATC
 AGAAATATTGATCCATGTGCACGCAGATAAAATGGCTTCTGCTAAACAGACTAAAATCTTTCTCTAGTCTTTT
 TCACTTGTACAAACCCAGTTTGTTTTCAAAAAATCACAGTAGCAATGCAACTCATCACTCTAGAAAAGCAAGCTT
 AGGCTACCTGAAAGATTTTCCCTTGGAAGTTTAGCGTATGTTGACTAACAAAAATTCCCTACATCAGAGACTCT
 AGGTGCTATATAATCCAAAACTTTTCAGCCTGTTGCTCATTCTGTCCCATGCTGGCAATAATACCTTGTGAGCC
 CATTACCCTTATTTTGAATTGCTCCATCTCCTGGTGGGACTTGTATCTTGTCTGCCATATCAGAACACAAACCCC
 TGAAGAGGTTCTGATTTGATTTTTTTTTTTTCTTCATGCCTACCCTTTTTTTTGAAGTTTCCAGCCGCAATTTGA
 AATGAAATGACAAGGTGTATATTTGATCAATTTTCATTCCCACCATTGCATTACAACCTCTAACTTAAATGGGTA
 ACCCTAAGGCATATCAAAGAAGCAGATTGCATGATAAACGGAAATAGAAAAAAGAACCTACATTTATTTTGCTT
 TAGCATCCTTACTCTCACCTTTTATGAGATTGAGAGTGGACTTACATTTCTTTTTTACATTTTCTGATATTTAT
 TTTTTTTAGCCATCATTATATGTTTAAGTCTATTATGGGCAACCAATCTTTGGAAGCTGAAAACCTGAATTTAAAG
 AATGCTATCTTGAAAATTGCATACGTCTGTGCAATTTTTTATTCTGCCTAGTGCTATTCTGCTTGTTTAACTAG
 ATTGTACAAAATAAATTTCATTGCTTAATATCAAATTACAAAGTTTAGACTTGGAGGGAAATGGGCTTTTTTAGAAG
 CAAACAATTTTAAATATATTTTGTCTTCAAATAAATAGTGTTTAAACATTGAATGTGTTTTGTGAACAATATCC
 CACTTTGCAAACCTTTAACTACACATGCTTGAATTAAGTTTTAGCTGTTTTTATTGCTCAATAATAAAGCCTGAA
 TTCTGATCAATAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA

FIGURE 6

MKKVLLLLITAILAVAVGFPVSQDQEREKRSISDSDELASGFFVFPPYPYPPFRPLPPIPFPRFPWFRNFPPIPIPES
APTTPLPSEK

Signal sequence.

amino acids 1-17

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FIGURE 7

MRPQGPAASPQRLRGLLLLLLLQLPAPSSASEIPKGGKQKAQLRQREVVDLYNGMCLQGPAGVPGRDGSPGANVIP
GTPGIPGRDGFKEGKEGECRESFEESWTPNYKQCSWSSLNYGIDLKIAECTFTKMRSNSALRVLFSGSLRLKCR
NACCQRWYFTFNGAECSGPLPIEAIITYLDQGSPEMNSTINIHRTSSVEGLCEGIGAGLVDVAIWVGTCSDYPKGD
ASTGWNSVSRIIIEELPK

Signal sequence.

amino acids 1-30

N-glycosylation site.

amino acids 186-189

N-myristoylation sites.

amino acids 67-72, 117-122, 163-168, 199-204, 203-208

FIGURE 8

MENPSPAAALGKALCALLLATLGAAGQPLGGESICSARAPAKYSITFTGKWSQTAFPKQYPLFRPPAQWSSLLGA
 AHSSDYSMWKRKNQYVSNGLRDFAEERGEAWALMKEIEAAGEALQSVHEVFSAPAVPSGTGQTSAELEVQRRHSLVS
 FVVRIVPSPDWFVGVDSLDLCDGDRWREQAALDLYPYDAGTDSGFTFSSPNFATIPQDTVTEITSSSPSHPANSE
 YYPRLKALPPIARVTLLRLRQSPRAFIPAPVLPSPRDNEIVDSASVPETPLDCEVSLWSSWGLCGGHCGRGLGTS
 RTRYVRVQPANNGSPCPELEEEAECPDNCV

Signal sequence.

amino acids 1-26

Glycosaminoglycan attachment site.

amino acids 131-134

cAMP- and cGMP-dependent protein kinase phosphorylation site.

amino acids 144-147

N-myristoylation sites.

amino acids 26-31, 74-79, 132-137, 134-139, 190-195, 287-292, 290-295

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FIGURE 9

MGVWLNKDDYIRDLKRIILCFLIVYMAILVGTDQDFYSL LGVSKTASSREIRQAFKKLALKLHPDKNPNNPNAHG
 DFLKINRAYEVLKDEDLRKKYDKYGEKLEDNQGGQYESWNYRYDFGIYDDDPEIITLERREFDAAVNSGELWF
 VNFYSPGCSHCHDLAPTWRDFAKEVDGLLRIGAVNCGDDRLCRMKGVNSYPSLFIFRSGMAPVKYHGDRSKESL
 VSFAMQHVRSVTTELWTGNFVNSIQTAFAAGIGWLITFC SKGGDCLTSQTRLRLSGMLFLNSLDAKEIYLEVIHN
 LPDFELLSANTLEDRLAHRWLLFFHFGKNENSNDPELKKLKTLLKNDHIQVGRFDCSSAPDICSNLYVFQPSLA
 VFKGQGTKEYEIHGKKILYDILAFAKESVNSHVTTLGPQNFPANDKEPWLVDFFAPWCPPCRALLPELRRASNL
 LYGQLKFGTLDCTVHEGLCNMYNIQAYPTTVVFNQSNIEHEGHS AEQILEFIEDLMNPSVVSLTPTTFNELVT
 QRKHNEVVMVDFYSPWCHPCQVLMPEWKRMARTLTGLINVGSIDCQQYHSFCAQENVQRYPEIRFFPPKSNKAYQ
 YHSYNGWNRDAYSLRIWGLGFLPQVSTDLTPQTFSEKVLQGNHWVIDFYAPWCGPCQNFAPFELLARMIKGKV
 KAGKVDCQAYAQTCQKAGIRAYPTVKFYFYERAKRNFQEEQINTRDAKAI AALISEKLETLRNQGRNKDEL

Signal sequence.

amino acids 1-48

N-glycosylation site.

amino acids 484-487

cAMP- and cGMP-dependent protein kinase phosphorylation site.

amino acids 445-448

N-myristoylation sites.amino acids 2-7, 41-46, 103-108, 110-115, 157-162, 182-187, 243-248, 458-463,
566-571**Amidation sites.**

amino acids 389-392, 739-742

Endoplasmic reticulum targeting sequence.

amino acids 744-748

Cytochrome c family heme-binding site signature.

amino acids 158-163

Thioredoxin.

amino acids 128-234, 406-509, 511-592, 623-703

DnaJ domain.

amino acids 35-100

FIGURE 10

MAQQACPRAMAKNGLVICILVITLLLDQTTSHTSRLKARKHSKRRVRDKDGD LKTQIEKLWTEVNALKEIQALQT
VCLRGTKVHKKCYLASEGLKHFHEANEDCISKGGILVIPRNSDEINALQDYGKRSLPGVNDEFWLGINDMVTEGKF
VDVNGIAISFLNWDRAQPNGGKRENCVLFSSQAQGKWSDEACRSSKRYICEFTIPK

Signal peptide.

amino acids 1-31

N-myristoylation sites.

amino acids 14-20, 155-161

Amidation sites.

amino acids 126-130, 170-174

C-type lectin domain signature.

amino acids 176-201

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